

PROPIONIC AND METHYLMALONIC ACIDEMIAS: A HISTORICAL REVIEW

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ABSTRACT

Methylmalonic and propionic acidemia are two organic acidemias. These inborn errors of amino acid metabolism have been studied extensively for decades. Through clinical and scientific study, researchers have been able to elucidate the biochemistry and cell biology that underlies these two diseases. This review gives a comprehensive overview of the history of the disease, as well as a scientific description of the related enzymes, cofactors, and genetic basis for disease. In conclusion, clinical manifestations and treatments are described, and recommendations for further study are provided.

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INTRODUCTION

Branch chain amino acid metabolism has been a topic of study for researchers for decades. In studying branch chain amino acid metabolism, scientists have found many inborn errors of metabolism that cause disease. In examining both the pathways and the disease states, a full picture of the biochemistry behind branch chain amino acid metabolism can be elucidated.

Methylmalonic acidemia and propionic acidemia are two diseases that occur as a result of inborn errors of branch chain amino acid metabolism. Propionic acidemia was first described by Childs¹ in 1961, and was originally called ketotic hyperglycinemia. With continued research, it was discovered that the disease was an error of propionate metabolism that often, but not always, had ketosis and hyperglycinemia as clinical features. The next year, Cox and White² described methylmalonic acidemia as a metabolic error that manifests in some patients when serum cobalamin (B12) levels are low. Cox and White also showed that cobalamin administration would alleviate methylmalonic acid levels in a single patient. Today it is understood that this patient did not have classical methylmalonic acidemia where the inborn error is found in methylmalonyl-CoA mutase, rather, he had a defect in cobalamin synthesis. Much work has been done in the last decades to understand the biochemical, genetic, and clinical components of these two diseases.

BIOCHEMISTRY

Propionate metabolism has been elucidated by studying animal and human tissues, primarily liver and kidney. In 1955, Lardy³ showed that propionate is converted to succinate by enzymes in liver mitochondria in a range of animals. That same year, it was also reported by two groups that methylmalonate is an intermediate in propionate metabolism.^{4,5} Additional studies confirmed that methylmalonyl-CoA was converted to succinyl-CoA.⁶ Two years later, Flavin's group described a more complete sequence of propionate metabolism that included appropriate CoA esters.⁷

Methylmalonate as an intermediate was further shown to have two isomeric forms. In 1964⁸, it was shown that the "D" form of methylmalonyl-CoA was formed directly from propionyl-CoA carboxylase. However, two years later, Sprecher⁹ reported that methylmalonyl-CoA must be converted to its L-isoform in order to be converted to succinyl-CoA by methylmalonyl-CoA mutase. Meanwhile, Mazumder had isolated and purified methylmalonyl-CoA racemase from sheep liver, and had also determined that the racemization occurred by an α -hydrogen atom shift.¹⁰ Thus, the components of the pathway were completely described.

Propionyl-CoA \rightarrow D-methylmalonyl-CoA \rightarrow L-methylmalonyl-CoA \rightarrow Succinyl-CoA \rightarrow Succinate

PROPIONATE SOURCES

Propionate is found in small quantities in the human body. It is an important part of amino acid metabolism, and is part of a pathway that eventually feeds into the citric acid cycle via succinyl-CoA. Propionate comes from three important sources in the body: anaerobic gut bacteria, branch chain amino acid metabolism, and β -oxidation of odd-numbered long chain fatty acids. In methylmalonic acidemia and propionic acidemia patients, the proportion of propionate generated from each source is somewhere around 50% from amino acids, and either 20%/30% bacteria/fatty acids¹¹ or 25%/25% bacteria/fatty acids.¹²

Childs¹ first described the amino acids that may play a role in producing propionyl-CoA. His studies implicated leucine, and to a lesser degree isoleucine, valine, and threonine. For methylmalonic acidemia, Rosenberg²⁶ implicated isoleucine and valine as disease causing. Interestingly it was 1975 before the full biochemical pathway was determined that showed that propionate was an intermediate of valine metabolism.^{13, 14} It is now known definitively that isoleucine and valine metabolism are the leading amino acids that contribute to disease via propionyl-CoA formation.

ENZYMES

During the period that the biochemical pathways were being elucidated, the enzymes responsible for the reactions within the pathways were also being discovered, isolated, and purified.

Propionyl-CoA carboxylase was first described by Tietz¹⁵ in 1959, where he described the mechanism of this enzyme, which included performing both CO₂ activation and carboxylation activities. Later, propionyl-CoA carboxylase was first crystallized in pig's heart and also shown to bind biotin.¹⁶ Studies crystallizing the enzyme from bovine kidney¹⁷ and human liver confirmed this.^{18, 19} Propionyl-CoA carboxylase is composed of 2 non-identical subunit protomers¹⁷, the larger of which binds biotin.^{15, 17} The human enzyme is 750-800 kDalton in its native form,²⁰ and the mass of each subunit is 72 kDalton and 56 kDalton for the α and β subunits, respectively.¹⁹ In conjunction with this data, it was also shown that the homologous enzyme in the bacterium *Mycobacterium smegmatis* has a $(\alpha\beta)_6$ configuration.²¹ All of this evidence points to an $(\alpha\beta)_6$ configuration for the human enzyme as well.

The CO₂ fixation and the carboxylase activity of propionyl-CoA carboxylase happen in tandem. ATP is required and potassium²² stimulates the first step which is forming a carboxybiotin-apoenzyme complex. The resulting complex reacts directly with the biotin in order to transfer the carboxyl group, forming methylmalonyl-CoA.²³ The biotin is directly linked to a well-defined biotin binding site on the α -subunit.²⁴

Methylmalonyl-CoA mutase was described in 1959, as an enzyme analogous to β -methylaspartate in bacteria.²⁵ It was also shown to require B12 (in the form

adenosylcobalamin) at this time.²⁶ Isolation and purification of methylmalonyl-CoA mutase from human placenta showed that it is a dimer composed of identical subunits.²⁷ Methylmalonyl-CoA mutase is covalently bonded to B12, which is a fact confirmed by isolation of methylmalonyl-CoA mutase from human liver.²⁸ It was demonstrated that activity of the enzyme was stimulated by anions, and inhibited by cations. In addition, hydroxocobalamin, a form of cobalamin, was found to be an irreversible and competitive inhibitor of the enzyme.²⁹ The enzyme is a homodimer with the molecular mass of 145 kDaltons, and each subunit binds one cobalamin. This is in contrast to the methylmalonyl-CoA mutase found in *Propionibacterium shermanii*, which is made of 2 non-identical subunits, where the α -subunit binds adenosylcobalamin. The human form of the enzyme appears to have unequal binding sites, as it has been shown to have complex kinetics.²⁹

The mechanism by which methylmalonic-CoA mutase works is by an intramolecular shift of the CoA carboxyl group.^{30, 31} This shift occurs via a pair of free radicals formed by adenosylcobalamin.³² Electron paramagnetic resonance studies confirmed this mechanism by showing the radical intermediates that are formed from the homolytic dissociation of the adenosylcobalamin cobalt-carbon bond.³³ *Propionibacterium shermanii* also showed radical intermediates by electron paramagnetic resonance, which is further proof of this mechanism.³⁴ Additionally UV-stopped flow spectroscopy shows that the homolysis is coupled to hydrogen atom extraction from methylmalonyl-CoA, not adenosylcobalamin.³⁵

COFACTORS

Propionyl-CoA carboxylase requires biotin as a cofactor. Kogl first isolated biotin from egg white.³⁶ The structure of biotin was determined in 1942.³⁷ Biotin binds to the lysine of a well-defined binding site that has the sequence Ala-Met-Lys-Met.^{24,38} Propionyl-CoA carboxylase is biotinylated by holocarboxylase synthetase.³⁹

Methylmalonyl-CoA mutase requires cobalamin as a cofactor^{40,41,42}; more specifically the mutase requires a form of cobalamin called adenosylcobalamin. Cobalamin was first determined to be of interest in 1926 when Minot and Murphy⁴³ successfully treated pernicious anemia with a diet that included crude liver extracts. Two decades later, crude liver extract was again examined, and cobalamin isolated.⁴⁴ Rickes crystallized cobalamin from liver that same year, and also named it vitamin B12.⁴⁵ The structure of cobalamin was determined soon after by electron density mapping.⁴⁶ Cobalamin has many forms, but only the form adenosylcobalamin acts as a cofactor for methylmalonyl-CoA mutase.²⁵ The pathway from cobalamin to adenosylcobalamin was first described in *Clostridium tetanomorphum*, where it was also shown that magnesium was required.⁴⁷ It was later confirmed that a similar pathway occurs in mammals, as was shown by looking at the liver and kidneys of rabbit, rat, and human.⁴⁸ Kerwar also showed that cobalamin could be converted to adenosylcobalamin by HeLa cells, so long as they were cultured in the presence of ATP and in a reducing system.⁴⁹ This set of experiments also showed that the synthesis and cofactor activity was present in mitochondria.

GENE AND PROTEIN STRUCTURE

In 1986, the cDNA for propionyl-CoA carboxylase was first isolated.⁵⁰ Lamhonwah showed that the gene *PCCA*, responsible for propionyl-CoA carboxylase subunit α , was on chromosome 13; additionally, the gene *PCCB*, encoding propionyl-CoA carboxylase subunit β was on chromosome 3. This was further narrowed to *PCCA* being located at 13q32, and *PCCB* at 3q22.⁵¹ They also noted that the α subunit mRNA was much larger than the β -subunit mRNA, with transcript lengths of 2.9 kb and 2.0 kb, respectively. The following year, a partial cDNA sequence was published, which showed the sequence for the biotin binding site and an approximately 60 amino acid conserved region that included the biotin binding site.⁵² Other groups also published information gleaned about the individual subunits α ^{53, 54} and β ^{55, 56, 57, 58, 59}, such as sequence fragments, amino acid length, exon boundaries, and pre- and post-processing size of the protein. The full cDNA sequence of each subunit was published soon after, which, for each, showed the complete structure of the 5'UTR, 3'UTR, and mitochondrial leader sequence.⁶⁰ Additional studies showed that the two subunits had unequal rates of synthesis or degradation, with the β -subunit being in excess.⁶¹

The methylmalonyl-CoA mutase gene was cloned in 1988 from human placenta.⁶² The next year, this data was confirmed by cloning cDNA from human liver.⁶³ They showed that methylmalonyl-CoA mutase has a 742 amino acid open reading frame and a 32 amino acid leader sequence. Methylmalonyl-CoA mutase was shown to be located on chromosome 6, in the p12-21.1 region.^{64, 65} The mutase is 13 exons long, and spans more than 35 kb of the genome. In 1986, Rosenberg also showed the mitochondrial targeting

sequence in detail, noting that it had a net positive charge, and that cleavage took place between a glutamine and an asparagine.⁶⁶ The trafficking of methylmalonyl-CoA mutase into the mitochondria is modulated by an energy-dependent mechanism; once in the mitochondria it is quickly converted into its mature form.⁶⁷ The presence or absence of adenosylcobalamin does not affect the localization of the mutase into the mitochondria.⁶⁸ The crystal structure of *Propionibacterium shermanii* shows that the C-terminal end is responsible for binding adenosylcobalamin, and the N-terminal end contains the homobinding domain.⁶⁹ The crystal structure of *Propionibacterium shermanii* has also helped elucidate how the cobalt atom is coordinated in the enzyme,⁷⁰ how methylmalonyl-CoA is found in bound and unbound forms⁷¹, and what the structure looks like with and without a tyrosine at the active site⁷².

CAUSE OF DISEASE STATES

Deficiencies resulting in disease

Cofactor deficiencies have been known to cause many different diseases. In the case of propionyl-CoA carboxylase, the cofactor is biotin. There is a report of experimental biotin deficiency⁷³ induced by biotin sequestration by consuming large amounts of egg white. The symptoms resulting from this diet were reversed with the application of biotin. Because methylmalonic acidemia has a cobalamin-responsive form (discussed below), it was postulated by Hsia that there might be a biotin responsive form of propionic acidemia.⁷⁴ However, there have been no reports of such a disease.

Methylmalonyl-CoA mutase requires the cofactor of adenosylcobalamin. There have been reports of cobalamin deficiency leading to methylmalonic acidemia.^{ii, iii, 75} Most cases were readily reversed when cobalamin was administered, though some patients did not respond to cobalamin treatment. This result implicated methylmalonyl-CoA mutase as an additional location for metabolic defect, along with cobalamin deficiency.⁹⁵ It was also reported that homocystinuria occurs in patients with cobalamin-responsive methylmalonic acidemia.^{76, 77} There has been one report of a child born with methylmalonic acidemia due to his vegetarian mother being cobalamin deficient during pregnancy.⁷⁸ The child was returned to health after cobalamin was added to his diet.

Genetic mutation resulting in disease

Retrospectively, Childsⁱ was the first to identify propionic acidemia as a new disease. This disease state was further confirmed in 1968.⁷⁹ Studies used ¹⁴C labeled propionate and showed that there was an error in propionate metabolism in patient fibroblasts⁸⁰ and leukocytes^{li}. While propionyl-CoA carboxylase was clearly implicated as having a defect, this wasn't confirmed genetically until 1990⁸¹ when the first of a slew of mutations were reported.^{82, 83, 84, 85, 86} In the α -subunit, these mutations included 2 short insertion/deletions creating an exon skip, an insertion creating a premature stop codon, and mutations reducing the stability of the protein. In the β -subunit, mutations were found^{81, 87, 88, 59} that cause the deletion of 14 basepairs with the insertion of 12 basepairs that creates a premature stop codon, an insertion leading to a premature stop codon, splicing mutations, and a mutation causing an exon skip. There is evidence for interallelic complementation with respect to the β -subunit.⁸⁹ The diversity in mutations that cause disease might be

responsible for the heterogeneity of symptoms and outcomes in propionic acidemia patients. Propionic acidemia is inherited in an autosomal recessive manner.⁹⁰

There have been reports of patients who have a genetic defect in the enzyme that biotinylates propionyl-CoA carboxylase, holocarboxylase synthetase. Holocarboxylase synthetase also biotinylates Acetyl-CoA carboxylases 1 and 2, 3-methylcrotonyl-CoA carboxylase, pyruvate carboxylase.⁹¹ Because holocarboxylase synthetase biotinylates these three additional enzymes, additional pathways are also affected. These patients have the disease multiple carboxylase deficiency.⁹²

There has been one report of a patient with a methylmalonyl-CoA racemase deficiency.⁹³ This patient was restudied and confirmed to have a racemase mutation.⁹⁴

In methylmalonic acidemia, methylmalonyl-CoA mutase was implicated by Smith and Monty in 1959.⁴⁰ This was further postulated in 1967⁹⁵ and 1968⁹⁶, when researchers came across patients with symptoms that were similar to cobalamin responsive patients, however, these new patients did not respond to cobalamin treatment. Genetically, the first mutations were found in 1990 when cDNA was cloned and sequenced from a patient.⁹⁷ Also that year, it was noted that the patients described to date did not have gross chromosomal rearrangements, large insertions or deletions, or mutations at restriction enzyme sites.⁹⁸ Since then many mutations have been found throughout the gene that cause either a *mut*⁰ or *mut*⁻ phenotype.^{99, 100, 101, 102, 103} Interestingly, there are some *mut*⁰ cell lines that were able to complement some, but not all, *mut*⁰ lines, giving evidence of interallelic complementation.¹⁰⁴ Because methylmalonyl-CoA mutase from *Propionibacterium shermanii* shares 65% sequence identity with human methylmalonyl-

CoA mutase, it can be used as a model to map mutations.¹⁰⁵ As such, Thoma showed that of the 12 known mutations at the time, eight were in the C-terminal adenosylcobalamin binding domain, and four were in the N-terminal homobinding domain.⁶⁹ More recently, a patient has been found with a mutation that results in a lack of targeting sequence for the protein.¹⁰⁶ Lastly, all of the mutations reported are inherited in an autosomal recessive manner, as evidenced by roughly equal numbers of males and females affected and lack of direct parental transmission of the disease.^{95, 107} Many patients with methylmalonic acidemia are compound heterozygotes.¹⁰⁸

Early on, it was reported that in addition to mutase deficiencies, abnormalities in cobalamin synthesis could lead to clinically significant methylmalonic acidemia..¹⁰⁹ Cox and Whiteⁱⁱ were the first to report on a patient whose symptoms were alleviated with cobalamin treatment. This was the first hint that cobalamin metabolism could lead to disease. Additional studies^{110, 111} were done that showed that the primary defect in certain methylmalonic acidemia patients was in cobalamin metabolism. Early on it was known that there was more than one step that was affected, as 2 patients were shown to have different rates of accumulation of adenosylcobalamin, while retaining similar methylmalonyl-CoA to succinate turnover.¹¹¹ The first complementation tests showed that there were three complementation groups: *cblA*, *cblB*, and *cblC*.¹¹² Later studies confirmed the presence of a fourth group, *cblD*.¹¹³ Further complementation tests showed that *cblA* and *cblC* are mutants for NADPH- and NADH-aquacobalamin reductases.¹¹⁴ The *cblB* complementation group results from mutations in the cob(I)alamin adenosyltransferase.¹¹⁵ Complementation tests have shown that there is some interallelic

complementation within the *cblA* group.¹¹⁶ *cblA*, *cblB*, and *cblC* mutations are also inherited in an autosomal recessive manner.¹⁰⁷ More recently, *cblF* has been described.¹¹⁷ However, due to low patient numbers in the *cblD* and *cblF* groups, the mode of inheritance has not been described definitively.

DISEASE MANIFESTATIONS

Propionic Acidemia

Propionic acidemia was first described as ketotic hyperglycinemia.¹ This patient^{118, 119, 120, 121}, and his sister¹²² who was similarly affected, were studied extensively. The primary manifestations in these patients were vomiting, lethargy, ketosis, and hyperglycinemia. However, additional patients didn't consistently have the symptoms of ketosis¹²³, metabolic acidosis¹²⁴ or hyperglycinemia. In 1971, it was determined that ketotic hyperglycinemia and propionic acidemia were the same disease, and that the clinical presence of propionic acid, not ketosis or hyperglycinemia, was diagnostic for the disease.¹²⁵ A study of 65 cases revealed that the most common clinical symptoms were feeding difficulties, lethargy, and hypotonia, with less common symptoms of seizures, coma, and hepatomegaly, among others.⁹⁰ The hepatomegaly is due primarily to fat accumulation.⁷⁹ Long-term consequences include heart disease, metabolic stroke, pancreatitis, blindness, and hearing loss.

While propionic acidemia classically presents in the neonatal period, there are cases of “late onset” disease. Sutrees¹²⁶ compared those who presented early (within the

first week of life) with those who presented later (sixth week of life or later), and made the following observations. There was a higher death rate in the early onset group than the late onset group, each early onset patient had an IQ of less than 60 and many needed dialysis. In contrast, each of the late onset patients had an IQ of greater than 60, and movement disorders were common. Both groups had roughly equal proportion of patients with chorea and dystonia.

Patients with propionic acidemia have an characteristic biochemical profile including methylcitrate, propionylglycine, and 3-hydroxypropionate. Methylcitrate has been identified as a metabolite that was seen in patient, but not control populations.¹²⁷ Additionally, 3-hydroxypropionate has also been seen, which is likely a result of β -oxidation of propionate.¹²⁸ Tiglic aciduria has also been seen in patient samples.¹²⁹ Hyperammonemia is a common finding, and also correlates with propionic acid levels in serum.¹³⁰ It has been suggested that the hyperammonemia is due to propionic acid inhibiting ureagenesis when ammonia is the substrate.¹³¹ More specifically, it has been suggested that the hyperammonemia is either due to depletion of N-acetyl glutamate, which, in turn, is attributable to depletion of acetyl-CoA or it is due competitive inhibition by propionyl-CoA of N-acetyl glutamate synthetase.¹³² The latter hypothesis has been supported by additional studies.¹³³

There are other interesting, but inconsistent, findings in patients with propionic acidemia. Neurologic symptoms are common.¹³⁴ There are reports of fatal symmetric necrosis of the basal ganglia.^{124, 135} Additionally, there was a report of delayed neuronal

myelination upon inspection with an MRI.¹³⁶ One patient was also reported to have parathyroid hormone resistance and B-cell lymphopenia.¹³⁷

Alternatively, there have are reports of propionyl-CoA carboxylase deficiencies in people who are asymptomatic. Wolf reported on a child whose propionyl-CoA carboxylase deficiency was not found until she was 13, when her brother was found to be symptomatic. While her urine did not have an abnormal organic acid profile, her fibroblasts were shown to have less than 10% enzyme activity.¹³⁸ This is contrasted with a boy who was discovered after an affected sibling was found. His cultured fibroblasts showed only 3% enzyme activity, and he was found to excrete methylcitrate, 3-hydroxypropionate, and glycine similar to his brother and other propionic acidemia patients.¹³⁹

Methylmalonic Acidemia

Methylmalonic acidemia, the symptom, was first described in patients who had pernicious anemia, though pernicious anemia was a defect in cobalamin uptake and is distantly related to methylmalonic acidemia, the disease. Oberholzer showed that his patient excreted amounts of methylmalonic acid far in excess of pernicious anemia patients, and postulated that his patient had a new disease, which turned out to be methylmalonic acidemia due to a mutation in methylmalonyl-CoA mutase.⁹⁵ This was in contrast to cobalamin-responsive patients who had defects in cobalamin metabolism. However, cobalamin-responsive or not-responsive patients had similar symptoms. The two forms of the disease, cobalamin responsive and non-responsive, were described by Morrow in 1969.¹⁴⁰ He also stated that methylmalonic acid excretion was the hallmark of

this disease, and what differentiated it from ketotic hyperglycinemia (propionic acidemia). While methylmalonic acid excretion is a definitive diagnostic indicator for methylmalonic acidemia, studies show that excretion levels do not correlate with the clinical status of patients.¹⁴¹

Patients with methylmalonic acidemia present very similarly to patients with propionic acidemia. Symptoms include lethargy, failure to thrive, vomiting, dehydration, respiratory distress, hypotonia, and hepatomegaly.¹⁰⁷ More recently, patients with renal failure have been reported.^{142, 143} As with propionic acidemia, neurologic symptoms have been reported in methylmalonic acidemia.^{144, 145} Pancreatitis is also a chronic feature of this disease.¹⁴⁶ As noted earlier, there are two forms of methylmalonic acidemia due to methylmalonyl-CoA mutase defects, *mut*⁰ and *mut*⁻. Patients with *mut*⁰ mutations have a more severe disease course, and a higher death rate than *mut*⁻ patients.¹⁴⁷

Methylmalonic acidemia patients who have cobalamin metabolism deficiencies have similar presentation to patients with methylmalonyl-CoA mutase deficiencies, but usually have a later onset, less mortality, and less severe course of disease.¹⁴⁷

Biochemically, methylmalonic acidemia patients are also similar to propionic acidemia patients. Again, methylcitrate and 3-hydroxypropionate are seen,^{127, 128} as well as propionic acid¹⁴⁸ and its derivatives.¹⁴⁹ Additionally, methylmalonic acid is an inhibitor of the malate-phosphate exchange, which may be responsible for the common findings of hyperglycemia and ketonemia.¹⁵⁰ Because ketotic hyperglycinemia is seen in both methylmalonic acidemia and propionic acidemia, it must be a secondary effect of CoA

metabolism.¹⁵¹ Glutathione deficiency may contribute to lactic acidosis during decompensation episodes.¹⁵²

As with propionic acidemia, there have been reports of children with defects in methylmalonyl-CoA mutase and high methylmalonic acid levels who are asymptomatic.^{153, 154} All of these children were reported to have normal growth and development. Alternately, there was a report of a patient with “mild” methylmalonic acidemia, that is low-to-normal methylmalonic acid excretion, who had acidotic episodes and ketosis with hyperammonemia. Lastly, there have also been reports of children who have low-to-moderate methylmalonic acid excretion, as picked up by newborn screening, which usually resolved within two years of age.¹⁵⁵ Of those with persistent methylmalonic aciduria, but no metabolic episodes, all had normal somatic and cognitive outcomes.

DIAGNOSIS

Propionic acidemia and methylmalonic acidemia are usually diagnosed by measurement of their respective primary metabolite in urine or blood samples. However, prenatal testing has become available for both of these genetic disorders.

Propionic acidemia was first successfully diagnosed prenatally using cultured amniotic cells.¹⁵⁶ Propionyl-CoA carboxylase activity was not found in this culture, which was later confirmed using fibroblasts. Later, methylcitrate was used as a diagnostic marker in amniotic fluid.¹⁵⁷ Again, this was confirmed using propionyl-CoA carboxylase activity in cultured cells. Later, another prenatal diagnosis was made and

confirmed using chorionic villi.¹⁵⁸ Even more recently, acylcarnitines in amniotic fluid have been used as a diagnostic tool.¹⁵⁹

Methylmalonic acidemia was similarly diagnosed successfully *in utero*. Morrow first detected methylmalonic acid in maternal urine and used that as evidence for a diagnosis.¹⁶⁰ This diagnosis was confirmed at birth. He later used ¹⁴C incorporation in amniotic fluid cells to make a correct diagnosis.¹⁶¹ Mahoney similarly used cultured amniotic fluid cells, but also showed that amniotic fluid methylmalonic acid concentration was diagnostic.¹⁶²

TREATMENT

Prenatal treatment

With prenatal diagnosis comes the opportunity to start treatment. There have not been any reports of propionic acidemia being treated *in utero*. However, prenatal treatment of cobalamin responsive methylmalonic acidemia has been the subject of a few studies. In 1975, large doses of adenosylcobalamin were prescribed after culture of amniotic cells indicated a defect in cobalamin synthesis.¹⁶³ Additionally, another fetus, diagnosed in the third trimester responded well to large doses of adenosylcobalamin, as measured by maternal methylmalonic acid concentration.¹⁶⁴

Patient treatment

Traditionally, the goals of propionic acidemia treatment were to lower propionic acid levels, and regulate ammonia, glycine, and alanine levels. Peritoneal dialysis has been

used to successfully ameliorate some biochemical symptoms, such as hyperammonemia, of propionic acidemia.¹⁶⁵ Diet is an important source of controlling propionate precursors. As such, parenteral nutrition can be useful to control intake when the patient is having a metabolic crises.¹⁶⁶ When patients are not under metabolic stress, maintenance treatment options include protein restriction, biotin supplementation¹⁶⁷ and L-carnitine supplementation.¹⁶⁸ L-carnitine supplementation has been shown to increase the formation and excretion of short chain acylcarnitines and patients who were treated improved clinically.¹⁶⁹ Another study of carnitine supplementation in conjunction with glycine showed an increase in tolerated protein, increased weight, development, and muscle tone, while showing a decrease in ketosis and hyperammonemia.¹⁷⁰ Another option is antibiotic treatment to reduce the amount of propionate from anaerobic gut bacteria.¹⁷¹ In all patients, metronidazole was shown to reduce propionic acid excretion, and clinical improvement was seen in three of nine patients in this study.

Methylmalonic acidemia patients are treated similarly to propionic acid patients. Restriction of natural protein has been shown to require non-branch chain amino acid supplementation if the restriction is severe.¹⁷² Cobalamin is administered to those patients who have cobalamin-responsive disease. With protein restriction and cobalamin doses, patients have done well.¹⁷³ L-carnitine has also been prescribed for methylmalonic acidemia patients.¹⁶⁹ In one patient who took supplemental carnitine, hippurate, which is a measure of mitochondrial ATP and CoA availability, increased along with a decrease in methylmalonyl and methylcitrate excretion.¹⁷⁴ Antibiotic treatment has also been used to reduce the propionate formed by natural flora, and subsequently, methylmalonic acid

excretion levels.¹⁷⁵ An additional antibiotic study showed decreases in hydroxypropionate, methylcitrate, and odd-chain fatty acid levels.¹⁷⁶

Treatment of both acidemias has been largely supportive, and future studies should focus on finding improvements that impact patient health. Additionally, while the traditional method of restricting diet while administering carnitine and antibiotics has improved patient health¹⁷⁷, there is still a high probability of long-term complications.¹⁷⁸

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